```
ACGTTGACAC AGGAATGAAG AGTGTATTGG CTGAATCTTC AAGCAGAGGC GATATTGACC 60

ATGTGCTTTT TAAATTGGCC TGCGTGACCC GCCCACTTGG TGTAAAAGAA GAACCGGCCA 120

AAGGGAGGGC CTGAAGGACC TCCACAGGAG TGTGAGCAGC ACTGCTTCAG CAACAAAGCC 180

TCAGGTCCAC ATCTTGGGAA GAAT ATG GCC ACT TCC TGG GGG GCT GTC TTC     231
                           Met Ala Thr Ser Trp Gly Ala Val Phe
                            1               5

ATG CTG ATC ATA GCC TGC GTT GGC AGC ACT GTC TTC TAC AGA GAA CAG    279
Met Leu Ile Ile Ala Cys Val Gly Ser Thr Val Phe Tyr Arg Glu Gln
 10                  15                  20                  25

CAG ACC TGG TTT GAA GGT GTC TTC TTG TCT TCC ATG TGC CCC ATT AAT    327
Gln Thr Trp Phe Glu Gly Val Phe Leu Ser Ser Met Cys Pro Ile Asn
                 30                  35                  40

GTC AGT GCC GGC ACC TTT TAT GGA ATT ATG TTT GAT GCG GGC AGC ACT    375
Val Ser Ala Gly Thr Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr
             45                  50                  55

GGA GCT CGG ATT CAT GTT TAC ACT TTT GTG CAG AAA ACA GCA GGA CAG    423
Gly Ala Arg Ile His Val Tyr Thr Phe Val Gln Lys Thr Ala Gly Gln
         60                  65                  70
```

FIG. 1A

```
ctc ccc ttt ctg gaa ggt gaa att ttt gat tct gtg aag ccg gga ctt    471
Leu Pro Phe Leu Glu Gly Glu Ile Phe Asp Ser Val Lys Pro Gly Leu
     75                  80                  85

TCT GCT TTT GTG GAT CAG CCC AAA CAG GGT GCT GAG ACT GTC CAG GAG    519
Ser Ala Phe Val Asp Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Glu
 90                  95                 100                 105

CTC TTG GAG GTG GCC AAA GAC TCG ATC CCC AGA AGC CAC TGG GAA AGG    567
Leu Leu Glu Val Ala Lys Asp Ser Ile Pro Arg Ser His Trp Glu Arg
                110                 115                 120

ACC CCG GTG GTT CTG AAA GCA ACG GCC GGA CTC CGT TTG CTG CCT GAG    615
Thr Pro Val Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu
            125                 130                 135

CAG AAA GCC CAG GCT CTG CTC TTG GAG GTA GAG GAG ATC TTC AAG AAT    663
Gln Lys Ala Gln Ala Leu Leu Leu Glu Val Glu Glu Ile Phe Lys Asn
        140                 145                 150

TCA CCT TTC CTG GTC CCA GAT GGC AGC GTT AGC ATC ATG GAT GGG TCC    711
Ser Pro Phe Leu Val Pro Asp Gly Ser Val Ser Ile Met Asp Gly Ser
    155                 160                 165
```

FIG. 1B

```
TAT GAA GGC ATA CTA GCC TGG GTT ACC GTG AAC TTT CTA ACA GGT CAG    759
Tyr Glu Gly Ile Leu Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln
170                 175                 180                 185

CTG CAT GGT CGT GGC CAG GAG ACT GTG GGG ACC CTT GAC CTG GGG GGT    807
Leu His Gly Arg Gly Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly
                190                 195                 200

GCC TCC ACC CAA ATC ACG TTT CTA CCC CAG TTT GAG AAA ACC CTG GAA    855
Ala Ser Thr Gln Ile Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu
            205                 210                 215

CAA ACA CCT AGG GGC TAC CTC ACT TCC TTT GAG ATG TTT AAC AGC ACT    903
Gln Thr Pro Arg Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr
        220                 225                 230

TTT AAG CTC TAT ACA CAT AGT TAC TTG GGA TTT GGA CTG AAA GCT GCA    951
Phe Lys Leu Tyr Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala
    235                 240                 245

AGA CTG GCA ACT CTG GGA GCC CTG GAA GCA AAA GGG ACT GAT GGA CAT    999
Arg Leu Ala Thr Leu Gly Ala Leu Glu Ala Lys Gly Thr Asp Gly His
250                 255                 260                 265
```

FIG. 1C

```
ACG TTT CGA AGT GCC TGT TTA CCA AGA TGG TTG GAA GCA GAG TGG ATC   1047
Thr Phe Arg Ser Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile
                270                 275                 280

TTT GGG GGT GTG AAA TAC CAG TAT GGT GGT AAC CAA GAA GGG GAG ATG   1095
Phe Gly Gly Val Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Met
            285                 290                 295

GGC TTT GAA CCC TGC TAT GCG GAA GTG CTG AGG GTA GTA CAG GGG AAA   1143
Gly Phe Glu Pro Cys Tyr Ala Glu Val Leu Arg Val Val Gln Gly Lys
        300                 305                 310

CTT CAC CAG CCA GAA GAA GTC CGA GGA AGC GCC TTC TAC GCT TTC TCT   1191
Leu His Gln Pro Glu Glu Val Arg Gly Ser Ala Phe Tyr Ala Phe Ser
    315                 320                 325

TAC TAC TAC GAT CGA GCC GCT GAC ACA CAC TTG ATC GAT TAT GAA AAG   1239
Tyr Tyr Tyr Asp Arg Ala Ala Asp Thr His Leu Ile Asp Tyr Glu Lys
330                 335                 340                 345

GGC GGG GTT TTA AAA GTT GAA GAT TTT GAA AGA AAA GCC AGA GAA GTG   1287
Gly Gly Val Leu Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val
                350                 355                 360
```

FIG. 1D

```
TGT GAC AAC TTG GGG AGC TTC TCC TCG GGC AGT CCT TTC CTC TGC ATG   1335
Cys Asp Asn Leu Gly Ser Phe Ser Ser Gly Ser Pro Phe Leu Cys Met
            365                 370                 375

GAC CTC ACT TAC ATC ACA GCC CTG TTG AAA GAT GGT TTG GGC TTT GCC   1383
Asp Leu Thr Tyr Ile Thr Ala Leu Leu Lys Asp Gly Leu Gly Phe Ala
        380                 385                 390

GAA CGG CAC CCT CTT ACA GCT CAC AAA GAA AGT GAA CAA CAT AGA GAC   1431
Glu Arg His Pro Leu Thr Ala His Lys Glu Ser Glu Gln His Arg Asp
    395                 400                 405

TGG TTG GGC CTT GGG GGC CAC CTT TCA CCT GCT CCA GTC TCT GGG CAT   1479
Trp Leu Gly Leu Gly Gly His Leu Ser Pro Ala Pro Val Ser Gly His
410                 415                 420                 425

CAC CAG CTG AGG CCA AGC TCC ACC TCT GAA GCC TGC ATT TCT GAA CCA   1527
His Gln Leu Arg Pro Ser Ser Thr Ser Glu Ala Cys Ile Ser Glu Pro
                430                 435                 440

GTT TTC TCA CAG GAA GGC GTG GAC TCA GAG ACA TTT TCT GAC CTC TCT   1575
Val Phe Ser Gln Glu Gly Val Asp Ser Glu Thr Phe Ser Asp Leu Ser
            445                 450                 455
```

FIG. 1E

```
GGA AAA GCC TGG CCC GAA ACC CGT TAACTGGTTT TATAAGGAGG GAGGGGTTTT  1629
Gly Lys Ala Trp Pro Glu Thr Arg
        460                 465

TAGATGAGTC TTGCTCTTGA GCCTAGTGAT TTGGGCTTCA ATGATTTGCA CATCTAATGT 1689

GAATAGCTCC TAACCACTTG GTGGGTGCAT GGCTGGCACC AGACTGTAAA TCTTTTGGGA 1749

TTCTTTGTAC AGAGTCCTGC AAAGGAAAAA AGAGAAAAGG TTTGGAACTC CATGCTAGAT 1809

TGCGAGTTCA GAGACAGGTC CCTGGGGACC AAAGAACAAT CTCGTTTCAA CCCTTGGATG 1869

CCTCATTGCT TTGAATGGAT TCATTTTTGC TTATAAGCTG ATTTACTGAA ATCCCATAAC 1929

CCATCAATGC TGTTAATTTT TTTCTTCCTA CCCTTATTAC ATTCCCTACC CTAAAAGCCT 1989

GGGGGAAATA CCTGGTTTTG CTTCCCATCT ATAATTGAGA AAGAGGGGGG AAAAGATACT 2049

GTATTAGAAT TTGTGTGATC CTGTGGCACA ATAGATCAAC CAACCCATTT AAAGCTTAAA 2109

AAAAAAAAAA                                                        2119
```

FIG. 1F

```
peaNTPase   1    ----MELLIKLITFLLFSMPAITSSQYLGNNLLTSRKIFLKQEEISSYAVVFDAGSTGSR
potapyrase  1    MLNQNSHFIFIILAIFLVLPLSLLSKNVNAQIPLRRHLLSHESE--HYAVIFDAGSTGSR
mNTPase     1    MATSWGAVFMLIIACVGSTVFYREQQTWFEGVFLSSMCPINVSAGTFYGIMFDAGSTGTR
yGDPase     1    KTPEDISILPVNDEPGYLQDSKTEQNYPELADAVKSQTSQTCSEEHKYVIMIDAGSTGSR

peaNTPase   57   IHVYHFNQNLDLLHIGKGVEYYNKITPGLSSYANNPEQAAKSLIPLLEQAEDVVPDDLQP
potapyrase  59   VHVFRFDEKLGLLPIGNNIEYFMATEPGLSSYAEDPKAAANSLEPLLDGAEGVVPQELQS
mNTPase     61   IHVYTFVQKTAGQLPFLEGEIFDSVKPGLSAFVDQPKQGAETVQELLEVAKDSIPRSHWE
yGDPase     61   VHIYKFDVCTS--PPTLLDEKFDMLEPGLSSFDTDSVGAANSLDPLLKVAMNYVPIKARS

peaNTPase   117  KTPVRLGATAGLRLLNGDASEKILQSVRDMLSNRSTF-NVQPDAVSIIDGTQEGSYLWVT
potapyrase  119  ETPLELGATAGLRMLKGDAAEKILQAVRNLVKNQSTF-HSKDQWVTILDGTQEGSYMWAA
mNTPase     121  RTPVVLKATAGLRLLPEQKAQALLLEVEEIFKN-SPF-LVPDGSVSIMDGSYEGILAWVT
yGDPase     119  CTPVAVKATAGLRLLGDAKSSKILSAVRDHLEKDYPFPVVEGDGVSIMGGDEEGVFAWIT
```

FIG. 2A

```
peaNTPase  176  VNYALGNLGKKYTK--TVGVIDLGGGSVQMAYAVSKKTAKNAPKVADGDDPYIKKVVLKG
potapyrase 178  INYLLGNLGKDYKS--TTATIDLGGGSVQMAYAISNEQFAKAPQNEDG-EPYVQQKHLMS
mNTPase    179  VNFLTGQLHGRGQE--TVGTLDLGGASTQITFLPQFEK-----TLEQTPRGYLTSFEMFN
yGDPase    179  TNYLLGNIGANGPKLPTAAVFDLGGGSTQIVFEP---TFPINEKMVDGEHKF--DLKFGD

peaNTPase  234  IPYDLYVHSYLHFGREASRAEILKL------------------TPRSPNPCLLAGFNGIY
potapyrase 235  KDYNLYVHSYLNYGQLAGRAEIFKA------------------SRNESNPCALEGCDGYY
mNTPase    232  STFKLYTHSYLGFGLKAARLATLGA------------------LEAKGT----DGHTFRS
yGDPase    234  ENYTLYQFSHLGYGLKEGRNKVNSVLVENALKDGKILKGDNTKTHQLSSPCLPPKVNATN

peaNTPase  276  TYSGEEFKATAYTSGA-----NFNKCKNTIRKALKLNYPCPYQNCTFGGIWNGGGN---
potapyrase 277  SYGGVDYKVKAPKKGS-----SWKRCRRLTRHALKINAKCNIEECTFNGVWNGGGD---
mNTPase    270  ACLPRWLEAEWIFGGV-----KYQYGGNQEGEMGFEPCYAEVLRVVQGKLHQPEEVR---
yGDPase    294  EKVTLESKETYTIDFIGPDEPSGAQCRFLTDEILNKDAQCQSPPCSFNGVHQPSLVRTFK
```

FIG. 2B

```
peaNTPase   328  GQKNLFASSSFFYLPEDTGMVDASTPNFILRPVDIETKAKEACALNFEDAKSTYPFLDKK
potapyrase  329  GQKNIHASSFFYDIGAQVGIVDTKFPSALAKPIQYLNAAKVACQTNVADIKSIFPKTQDR
mNTPase     322  GSA-FYAFSYYYDRAADTHLIDYE-KGGVLKVEDFERKAREVCD-NLGSFSSGSP-----
yGDPase     354  ESNDIYIFSYFYDRTRPLGMPLSFTLNELNDLARIVCKGEETWNSVFSGIAGS---LDEL

peaNTPase   388  NVASYVCMDLIYQYVLLVDGFGLDPLQKITSGKEIEYQDAIVEAAWPLGNAVEAISALPK
potapyrase  389  NI-PYLCMDLIYEYTLLVDGFGLNPHKEITVIHDVQYKNYLVGAAWPLGCAIDLVSSTTN
mNTPase     374  ----FLCMDLTYITALLKDGLGFAERHPLTAHKESEQHRDWLGLGGHLSPAPVSGHHQLR
yGDPase     411  ESDSHFCLDLSFQVSLLHTGYDIPLQRELRTGKKIANKE----IGWCLGASLPLLKADNW

peaNTPase   448  FERLMYFV
potapyrase  448  KIRVASS*
mNTPase     430  PSSTSEACISEPVFSQEGVDSETFSDLSGKAWPETR*
yGDPase     467  KCKIQSA
```

FIG. 2C

```
                           ACR1
CD39       1  VKYGIVLDAGSSHTSLYIYKW-------PAEKENDTGV------VHQVEECRVK-GPGIS
ratCD39    1  VKYGIVLDAGSSHTNLYIYKW-------PAEKENDTGV------VQLLEECQVK-GPGIS
CD39L1     1  LKYGIVLDAGSSHTSMFIYKW-------PADKENDTGI------VGQHSSCDVP-GGGIS
chiATPase  1  FKYGIVLDAGSSHTAVFIYKW-------PADKENDTGV------VSEHSMCDVE-GPGIS
peaNTPase  1  SSYAVVFDAGSTGSRIHVYHF----------NQ-NLDLLHIGKGVEYYN----KITPGLS
potRROP1   1  EHYAVIFDAGSTGSRVHVFRF----------DE-KLGLLPIGNNIEYFM----ATEPGLS
yGDA1      1  HKYVIMIDAGSTGSRVHIYKF----------DVCTSP--PTLLD-EKFD----MLEPGLS
mNTPase    1  TFYGIMFDAGSTGTRIHVYTF----------VQKTAGQLPFLEG-EIFD----SVKPGLS
hCD39L2    1  -----------------------------------------------FK----ALKPGLS
celegans   1  IKYGVICDAGSSGTRLFVYTLKPLSGGL--TNIDT---L-----IHESEPVVKKVTPGLS
y71KD      1  DRFGIVIDAGSSGSRIHVFKWQDTESLLHATNQDSQSILQSVPHIHQEKDWTFKLNPGLS
```

FIG. 3A

ACR II

```
CD39       47  KF-VQKVNEIGI-YLTDCMERAREVIPR---S-QHQETPVYLGATAGMRLLRMESEELAD
ratCD39    47  KY-AQKTDEIAA-YLAECMKMSTERIPA---SKQHQ-TPVYLGATAGMRLLRMESKQSAD
CD39L1     47  SY-ADNPSGASQ-SLVGCLEQALQDVPK---ER-HAGTPLYLGATAGMRLLNLTNPEAST
chiATPase  47  SY-SSKPPAAGK-SLEHCLSQAMRDVPK---EK-HADTPLYLGATAGMRLLTIADPPSQT
peaNTPase  46  SY-ANNPEQAAKS-LIPLLEQAEDVVP----DDLQPKTPVRLGATAGLRLLN--GDA-SE
potRROP1   46  SY-AEDPKAAANS-LEPLLDGAEGVVP----QELQSETPLELGATAGLRMLK--GDA-AE
yGDA1      44  SFDTDSV-GAANS-LDPLLKVAMNYVPI----KARSCTPVAVKATAGLRLL---GDAKSS
mNTPase    46  AF-VDQPKQGAET-VQELLEVAKDSIPRSHWE--R--TPVVLKATAGLRLL---PEQKAQ
hCD39L2    10  AY-ADDVEKSAQG-IRELLDVAKQDIP---FDSGRP-TPLVLKATAGLRLL---PGEKAQ
celegans   51  SFG-DKPEQVVE-YLTPLLRFAEEHIPYEQLGE----TDLLIFATAGMRLL---PEAQKD
y71KD      61  SFE-KKPQDAYKSHIKPLLDFAKNIIPESHWSS----CPVFIQATAGMRLL---PQDIQS
```

FIG. 3B

ACR III

```
CD39       101  RVLDVVERSLSN-YPF-----DFQGARIITGQEEGAYGWITINYLLGKFSQKTRWFSIVP
ratCD39    101  EVLAAVSRSLKS-YPF-----DFQGAKIITGQEEGAYGWITINYLLGRFTQEQSWLNFIS
CD39L1     101  SVLMAVTHTLTQ-YPF-----DFRGARILSGQEEGVFGWVTANYLLENFI-KYGWVG--R
chiATPase  101  -CLSAVMATLKS-YPF-----DFGGAKILSGEEEGVFGWITANYLLENFI-KRGWLG--E
peaNTPase  97   KILQSVRDMLSNRSTFN-VQPD-A-VSIIDGTQEGSYLWVTVNYALGN-------L---G
potRROP1   97   KILQAVRNLVKNQSTFH--SKD-QWVTILDGTQEGSYMWAAINYLLGN-------L---G
yGDA1      95   KILSAVRDHLEKDYPFPVVEGD-G-VSIMGGDEEGVFAWITTNYLLGN-------IGANG
mNTPase    97   ALLLEVEEIF-KNSPF-LV-PD-GSVSIMDGSYEGILAWVTVNFLTGQ-------LHGRG
hCD39L2    61   KLLQKVKEYL-KHSPF-LV-GD-DCVSIMNGTDEGVSAWXTINFLTGS-------LKTPG
celegans   102  AIIKNLQNGLKSVTALRVSD---SNIRIIDGAWEGIYSWIAVNYILGR-------F-D--
y71KD      113  SILDGLCQGLKHPAEFLVEDCS-AQIQVIDGETEGLYGWLGLNYLYGH-------FNDYN
```

FIG. 3C

ACR IV

CD39	155	Y E T N N Q E T F G A L D L G G A S T Q V T F V P Q N Q
ratCD39	155	- D S Q K Q A T F G A L D L G G S S T Q V T F V P L N Q
CD39L1	152	W F R P R K G T L G A M D L G G A S T Q I T F E T T S P
chiATPase	151	W I Q S K K K T L G A M D F G G A S T Q I T F E T S D A I
peaNTPase	144	K K Y T K - - T V G V I D L G G G S V Q M A Y A V S K K
potRROP1	144	K D Y K S - - T T A T I D L G G G S V Q M A Y A I S N E
yGDA1	146	P K L - P - - T A A V F D L G G G S T Q I V F E P T F P I
mNTPase	146	Q E - - - - - T V G T L D L G G A S T Q I T F L P Q F E
hCD39L2	110	G S - - - - - S V G M L D L G G G S T Q I A F L P R V E
celegans	149	K E - N D S - K V G M I D M G G A S V Q I A F E I A - N E
y71KD	165	P E V S D H F T F G F M D M G G A S T Q I A F - - A P H D S

FIG. 3D

```
GTGGGGTCGT ATCCCGCGGG TGGAGGCCGG GGTGGCGCCG GCCGGGGCGG GGGAGCCCAA  60

AAGACCGGCT GCCGCCTGCT CCCCGGAAAA GGGCACTCGT CTCCGTGGGT GTGGCGGAGC 120

GCGCGGTGCA TGGAATGGGC TATGTGAATG AAAAAAGGTA TCCGTTATGA AACTTCCAGA 180

AAAACGAGCT ACATTTTTCA GCAGCCGCAG CACGGTCCTT GGCAAACAAG G ATG AGA  237
                                                        Met Arg
                                                          1

AAA ATA TCC AAC CAC GGG AGC CTG CGG GTG GCG AAG GTG GCA TAC CCC   285
Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro
            5                  10                  15

CTG GGG CTG TGT GTG GGC GTG TTC ATC TAT GTT GCC TAC ATC AAG TGG   333
Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp
     20                  25                  30

CAC CGG GCC ACC GCC ACC CAG GCC TTC TTC AGC ATC ACC AGG GCA GCC   381
His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala
 35                  40                  45                  50
```

FIG. 4A

```
CCG GGG GCC CGG TGG GGT CAG CAG GCC CAC AGC CCC CTG GGG ACA GCT    429
Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly Thr Ala
                 55                  60                  65

GCA GAC GGG CAC GAG GTC TTC TAC GGG ATC ATG TTT GAT GCA GGA AGC    477
Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser
             70                  75                  80

ACT GGC ACC CGA GTA CAC GTC TTC CAG TTC ACC CGG CCC CCC AGA GAA    525
Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu
         85                  90                  95

ACT CCC ACG TTA ACC CAC GAA ACC TTC AAA GCA GTG AAG CCA GGT CTT    573
Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu
    100                 105                 110

TCT GCC TAT GCT GAT GAT GTT GAA AAG AGC GCT CAG GGA ATC CGG GAA    621
Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu
115                 120                 125                 130
```

FIG. 4B

```
CTA CTG GAT GTT GCT AAA CAG GAC ATT CCG TTC GAC TTC TGG AAG GCC    669
Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala
                135                 140                 145

ACC CCT CTG GTC CTC AAG GCC ACA GCT GGC TTA CGC CTG TTA CCT GGA    717
Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly
            150                 155                 160

GAA AAG GCC CAG AAG TTA CTG CAG AAG GTG AAA GAA GTA TTT AAA GCA    765
Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe Lys Ala
        165                 170                 175

TCG CCT TTC CTT GTA GGG GAT GAC TGT GTT TCC ATC ATG AAC GGA ACA    813
Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn Gly Thr
    180                 185                 190

GAT GAA GGC GTT TCG GCG TGG ATC ACC ATC AAC TTC CTG ACA GGC AGC    861
Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser
195                 200                 205                 210

TTG AAA ACT CCA GGA GGG AGC AGC GTG GGC ATG CTG GAC TTG GGC GGA    909
Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly
                215                 220                 225
```

FIG. 4C

```
GGA TCC ACT CAG ATC GCC TTC CTG CCA CGC GTG GAG GGC ACC CTG CAG    957
Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln
            230                 235                 240

GCC TCC CCA CCC GGC TAC CTG ACG GCA CTG CGG ATG TTT AAC AGG ACC    1005
Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr
        245                 250                 255

TAC AAG CTC TAT TCC TAC AGC TAC CTC GGG CTC GGG CTG ATG TCG GCA    1053
Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met Ser Ala
    260                 265                 270

CGC CTG GCG ATC CTG GGC GGC GTG GAG GGG CAG CCT GCT AAG GAT GGA    1101
Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys Asp Gly
275                 280                 285                 290

AAG GAG TTG GTC AGC CCT TGC TTG TCT CCC AGT TTC AAA GGA GAG TGG    1149
Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp
                295                 300                 305

GAA CAC GCA GAA GTC ACG TAC AGG GTT TCA GGG CAG AAA GCA GCG GCA    1197
Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala
            310                 315                 320
```

FIG. 4D

```
AGC CTG CAC GAG CTG TGT GCT GCC AGA GTG TCA GAG GTC CTT CAA AAC   1245
Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn
        325                 330                 335

AGA GTG CAC AGG ACG GAG GAA GTG AAG CAT GTG GAC TTC TAT GCT TTC   1293
Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe
    340                 345                 350

TCC TAC TAT TAC GAC CTT GCA GCT GGT GTG GGC CTC ATA GAT GCG GAG   1341
Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu
355                 360                 365                 370

AAG GGA GGC AGC CTG GTG GTG GGG GAC TTC GAG ATC GCA GCC AAG TAC   1389
Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr
                375                 380                 385

GTG TGT CGG ACC CTG GAG ACA CAG CCG CAG AGC AGC CCC TTC TCA TGC   1437
Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys
            390                 395                 400

ATG GAC CTC ACC TAC GTC AGC CTG CTA CTC CAG GAG TTC GGC TTT CCC   1485
Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly Phe Pro
        405                 410                 415
```

FIG. 4E

```
AGG AGC AAA GTG CTG AAG CTC ACT CGG AAA ATT GAC AAT GTT GAG ACC   1533
Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr
    420                 425                 430

AGC TGG GCT CTG GGG GCC ATT TTT CAT TAC ATC GAC TCC CTG AAC AGA   1581
Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg
435                 440                 445                 450

CAG AAG AGT CCA GCC TCA TAGTGGCCGA GCCATCCCTG TCCCCGTCAG          1629
Gln Lys Ser Pro Ala Ser
                455

CAGTGTCTGT GTGTCTGCAT AAACCCTCCT GTCCTGGACG TGACTTCATC CTGAGGAGCC 1689

ACAGCACAGG CCGTGCTGGC ACTTTCTGCA CACTGGCTCT GGGACTTGCA GAAGGCCTGG 1749

TGCTGCCCTG GCATCAGCCT CTTCCAGTCA CATCTGGCCA GAGGGCTGTC TGGACCTGGG 1809

CCCTGCTCAA TGCCACCTGT CTGCCTGGGC TCCAAGTGGG CAGGACCAGG ACAGAACCAC 1869

AGGCACACAC TGAGGGGGCA GTGTGGCTCC CTGCCTGTCC CATCCCCATG CCCCGTCCGC 1929
```

FIG. 4F

```
GGGGCTGTGG CTGCTGCTGT GCATGTCCCT GCGATGGGAG TCTTGTCTCC CAGCCTGTCA 1989
GTTTCCTCCC CAGGGCAGAG CTCCCCTTCC TGCAAGAGTC TGGGAGGCGG TGCAGGCTGT 2049
CCTGGCTGCT CTGGGGAAGC CGAGGGACAG CCATAACACC CCCGGGACAG TAGGTCTGGG 2109
CGGCACCACT GGGAACTCTG GACTTGAGTG TGTTTGCTCT TCCTTGGGTA TGAATGTGTG 2169
AGTTCACCCA GAGGCCTGCT CTCCTCACAC ATTGTGTGGT TTGGGGTTAA TGATGGAGGG 2229
AGACACCTCT TCATAGACGG CAGGTGCCCA CCTTTCAGGG AGTCTCCCAG CATGGGCGGA 2289
TGCCGGGCAT GAGCTGCTGT AAACTATTTG TGGCTGTGCT GCTTGAGTGA CGTCTCTGTC 2349
GTGTGGGTGC CAAGTGCTTG TGTAGAAACT GTGTTCTGAG CCCCCTTTTC TGGACACCAA 2409
CTGTGTCCTG TGAATGTATC GCTACTGTGA GCTGTTCCCG CCTAGCCAGG GCCATGTCTT 2469
AGGTGCAGCT GTGCCACGGG TCAGCTGAGC CACAGTCCCA GAACCAAGCT CTCGGTGTCT 2529
```

FIG. 4G

```
CGGGCCACCA TCCGCCCACC TCGGGCTGAC CCCACCTCCT CCATGGACAG TGTGAGCCCC 2589
GGGCCGTGCA TCCTGCTCAG TGTGGCGTCA GTGTCGGGGC TGAGCCCCTT GAGCTGCTTC 2649
AGTGAATGTA CAGTGCCCGG CACGAGCTGA ACCTCATGTG TTCCACTCCC AATAAAAGGT 2709
TGACAGGGGC TTCTCCTTCA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA        2762
```

FIG. 4H

FIG. 5A

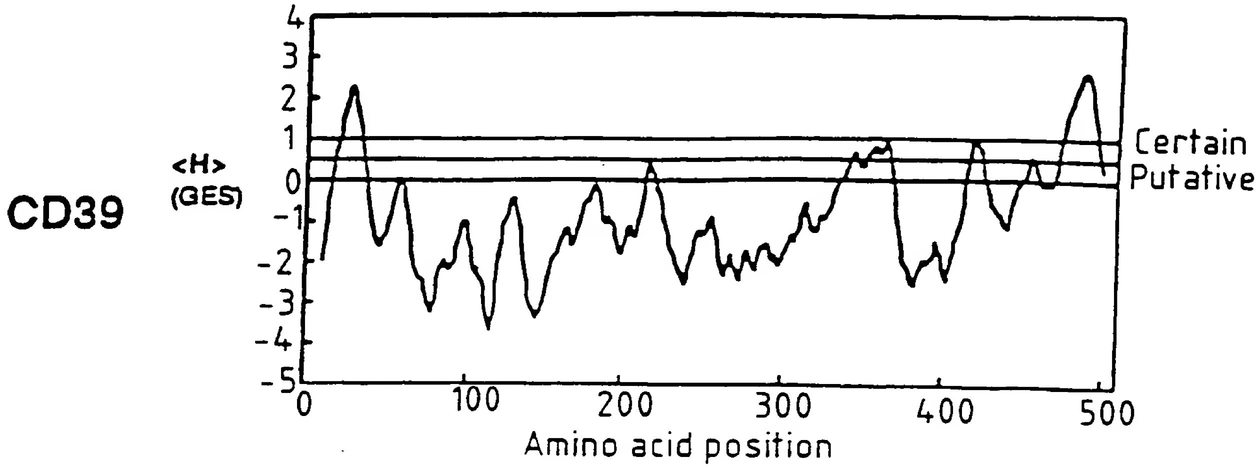


FIG. 5B

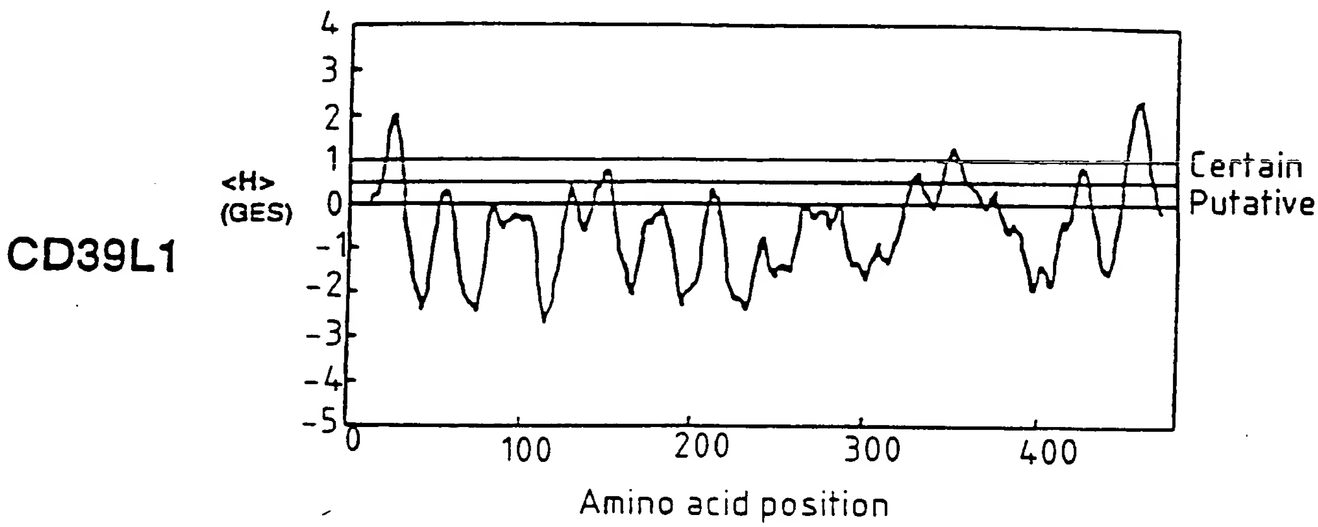


FIG. 5C

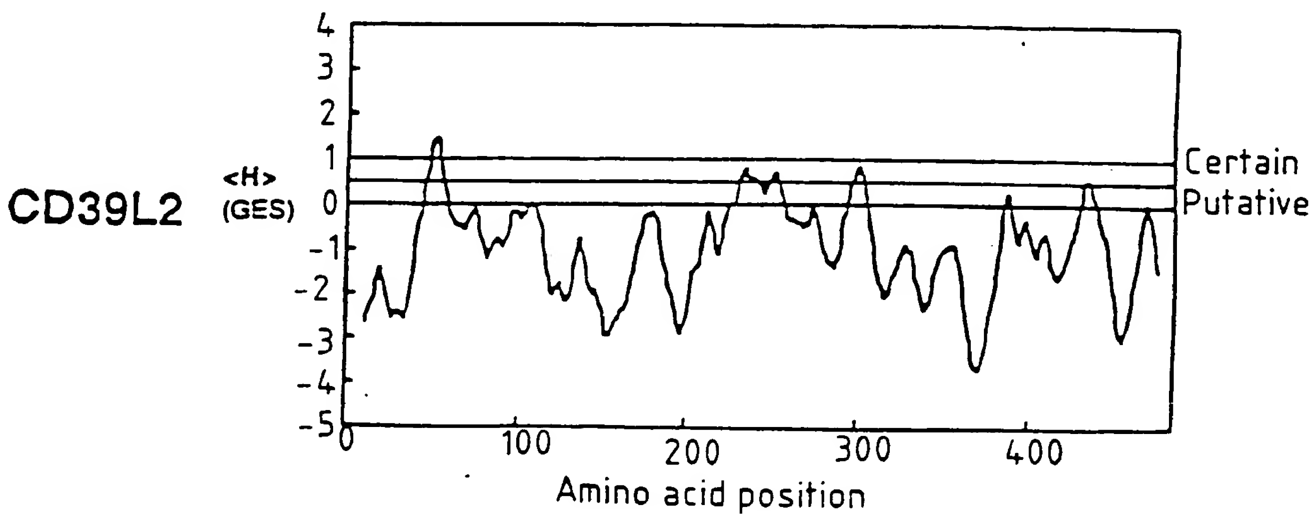


FIG. 5D

CD39L3

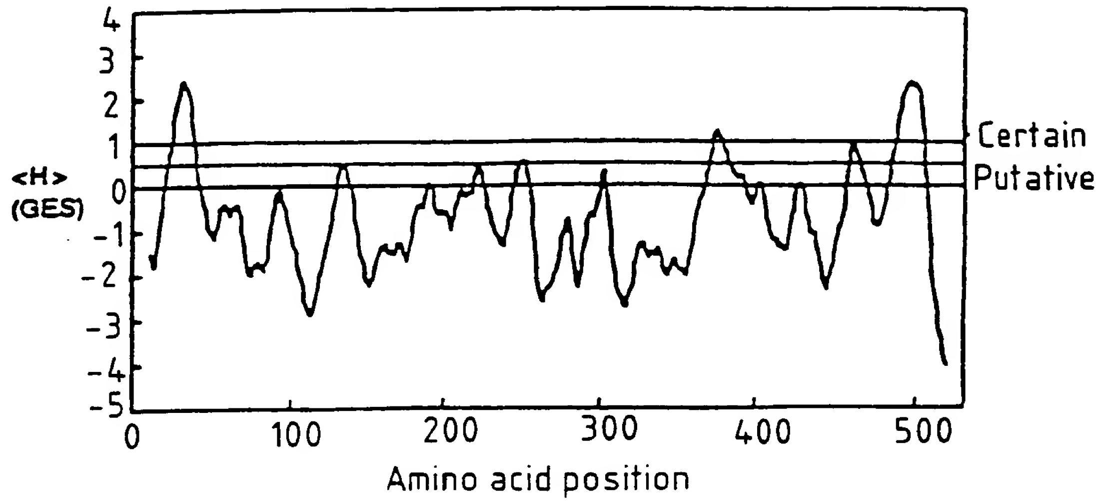
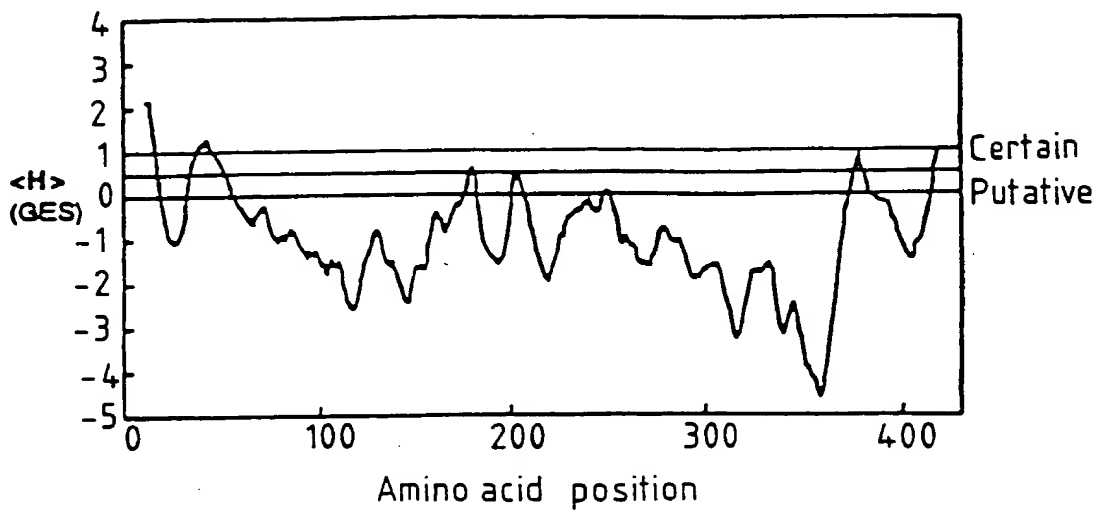


FIG. 5E

CD39L4



```
ACCCACGCGT CTGGCCGCGG GCCGCCTCTG CGGCAGCGCT AGTCGCCTTC TCCGAATCGG 60

CTCCGCACAG CTAGGAGAAA AG ATG TTC ACT GTG CTG ACC CGC CAA CCA TGT  112
                         Met Phe Thr Val Leu Thr Arg Gln Pro Cys
                          1               5                  10

GAG CAA GCA GGC CTC AAG GCC CTC TAC CGA ACT CCA ACC ATC ATT GCC  160
Glu Gln Ala Gly Leu Lys Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala
                15                  20                  25

TTG GTG GTC TTG CTT GTG AGT ATT GTG GTA CTT GTG AGT ATC ACT GTC  208
Leu Val Val Leu Leu Val Ser Ile Val Val Leu Val Ser Ile Thr Val
            30                  35                  40

ATC CAG ATC CAC AAG CAA GAG GTC CTC CCT CCA GGA CTG AAG TAT GGT  256
Ile Gln Ile His Lys Gln Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly
        45                  50                  55

ATT GTG CTG GAT GCC GGG TCT TCA AGA ACC ACA GTC TAC GTG TAT CAA  304
Ile Val Leu Asp Ala Gly Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln
    60                  65                  70
```

FIG. 6A

```
TGG CCA GCA GAA AAA GAG AAT AAT ACC GGA GTG GTC AGT CAA ACC TTC    352
Trp Pro Ala Glu Lys Glu Asn Asn Thr Gly Val Val Ser Gln Thr Phe
 75                  80                  85                  90

AAA TGT AGT GTG AAA GGC TCT GGA ATC TCC AGC TAT GGA AAT AAC CCC    400
Lys Cys Ser Val Lys Gly Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro
                 95                 100                 105

caa gat gtc ccc aga gcc ttt gag gag tgt atg caa aaa gtc aag ggg    448
Gln Asp Val Pro Arg Ala Phe Glu Glu Cys Met Gln Lys Val Lys Gly
            110                 115                 120

CAG GTT CCA TCC CAC CTC CAC GGA TCC ACC CCC ATT CAC CTG GGA GCC    496
Gln Val Pro Ser His Leu His Gly Ser Thr Pro Ile His Leu Gly Ala
        125                 130                 135

ACG GCT GGG ATG CGC TTG CTG AGG TTG CAA AAT GAA ACA GCA GCT AAT    544
Thr Ala Gly Met Arg Leu Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn
    140                 145                 150

GAA GTC CTT GAA AGC ATC CAA AGC TAC TTC AAG TCC CAG CCC TTT GAC    592
Glu Val Leu Glu Ser Ile Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp
155                 160                 165                 170
```

FIG. 6B

```
TTT AGG GGT GCT CAA ATC ATT TCT GGG CAA GAA GAA GGG GTA TAT GGA    640
Phe Arg Gly Ala Gln Ile Ile Ser Gly Gln Glu Glu Gly Val Tyr Gly
                175                 180                 185

TGG ATT ACA GCC AAC TAT TTA ATG GGA AAT TTC CTG GAG AAG AAC CTG    688
Trp Ile Thr Ala Asn Tyr Leu Met Gly Asn Phe Leu Glu Lys Asn Leu
            190                 195                 200

TGG CAC ATG TGG GTG CAC CCG CAT GGA GTG GAA ACC ACG GGT GCC CTG    736
Trp His Met Trp Val His Pro His Gly Val Glu Thr Thr Gly Ala Leu
        205                 210                 215

GAC TTA GGT GGT GCC TCC ACC CAA ATA TCC TTC GTG GCA GGA GAG AAG    784
Asp Leu Gly Gly Ala Ser Thr Gln Ile Ser Phe Val Ala Gly Glu Lys
    220                 225                 230

ATG GAT CTG AAC ACC AGC GAC ATC ATG CAG GTG TCC CTG TAT GGC TAC    832
Met Asp Leu Asn Thr Ser Asp Ile Met Gln Val Ser Leu Tyr Gly Tyr
235                 240                 245                 250

GTA TAC ACG CTC TAC ACA CAC AGC TTC CAG TGC TAT GGC CGG AAT GAG    880
Val Tyr Thr Leu Tyr Thr His Ser Phe Gln Cys Tyr Gly Arg Asn Glu
                255                 260                 265
```

FIG. 6C

```
GCT GAG AAG AAG TTT CTG GCA ATG CTC CTG CAG AAT TCT CCT ACC AAA    928
Ala Glu Lys Lys Phe Leu Ala Met Leu Leu Gln Asn Ser Pro Thr Lys
            270                 275                 280

AAC CAT CTC ACC AAT CCC TGT TAC CCT CGG GAT TAT AGC ATC AGC TTC    976
Asn His Leu Thr Asn Pro Cys Tyr Pro Arg Asp Tyr Ser Ile Ser Phe
        285                 290                 295

ACC ATG GGC CAT GTA TTT GAT AGC CTG TGC ACT GTG GAC CAG AGG CCA    1024
Thr Met Gly His Val Phe Asp Ser Leu Cys Thr Val Asp Gln Arg Pro
    300                 305                 310

GAA AGT TAT AAC CCC AAT GAT GTC ATC ACT TTT GAA GGA ACT GGG GAC    1072
Glu Ser Tyr Asn Pro Asn Asp Val Ile Thr Phe Glu Gly Thr Gly Asp
315                 320                 325                 330

CCA TCT CTG TGT AAG GAG AAG GTG GCT TCC ATA TTT GAC TTC AAA GCT    1120
Pro Ser Leu Cys Lys Glu Lys Val Ala Ser Ile Phe Asp Phe Lys Ala
                335                 340                 345

TGC CAT GAT CAA GAA ACC TGT TCT TTT GAT GGG GTT TAT CAG CCA AAG    1168
Cys His Asp Gln Glu Thr Cys Ser Phe Asp Gly Val Tyr Gln Pro Lys
            350                 355                 360
```

FIG. 6D

```
ATT AAA GGG CCA TTT GTG GCT TTT GCA GGA TTC TAC TAC ACA GCC AGT    1216
Ile Lys Gly Pro Phe Val Ala Phe Ala Gly Phe Tyr Tyr Thr Ala Ser
        365                 370                 375

GCT TTA AAT CTT TCA GGT AGC TTT TCC CTG GAC ACC TTC AAC TCC AGC    1264
Ala Leu Asn Leu Ser Gly Ser Phe Ser Leu Asp Thr Phe Asn Ser Ser
    380                 385                 390

ACC TGG AAT TTC TGC TCA CAG AAT TGG AGT CAG CTC CCA CTG CTG CTC    1312
Thr Trp Asn Phe Cys Ser Gln Asn Trp Ser Gln Leu Pro Leu Leu Leu
395                 400                 405                 410

CCC AAA TTT GAT GAG GTA TAT GCC CGC TCT TAC TGC TTC TCA GCC AAC    1360
Pro Lys Phe Asp Glu Val Tyr Ala Arg Ser Tyr Cys Phe Ser Ala Asn
                415                 420                 425

TAC ATC TAC CAC TTG TTT GTG AAC GGT TAC AAA TTC ACA GAG GAG ACT    1408
Tyr Ile Tyr His Leu Phe Val Asn Gly Tyr Lys Phe Thr Glu Glu Thr
            430                 435                 440

TGG CCC CAA ATA CAC TTT GAA AAA GAA GTG GGG AAT AGC AGC ATA GCC    1456
Trp Pro Gln Ile His Phe Glu Lys Glu Val Gly Asn Ser Ser Ile Ala
        445                 450                 455
```

FIG. 6E

```
TGG TCT CTT GGC TAC ATG CTC AGC CTG ACC AAC CAG ATC CCA GCT GAA   1504
Trp Ser Leu Gly Tyr Met Leu Ser Leu Thr Asn Gln Ile Pro Ala Glu
    460                 465                 470

AGC CCT CTG ATC CGT CTG CCC ATA GAA CCA CCT GTC TTT GTG GGC ACC   1552
Ser Pro Leu Ile Arg Leu Pro Ile Glu Pro Pro Val Phe Val Gly Thr
475                 480                 485                 490

CTC GCT TTC TTC ACA GTG GCA GCC TTG CTG TGT CTG GCA TTT CTT GCA   1600
Leu Ala Phe Phe Thr Val Ala Ala Leu Leu Cys Leu Ala Phe Leu Ala
                495                 500                 505

TAC CTG TGT TCA GCA ACC AGA AGA AAG AGG CAC TCC GAG CAT GCC TTT   1648
Tyr Leu Cys Ser Ala Thr Arg Arg Lys Arg His Ser Glu His Ala Phe
            510                 515                 520

GAC CAT GCA GTG GAT TCT GAC TGAGCCTTCA AAGCAGCTCC TGGAGTCCAA      1699
Asp His Ala Val Asp Ser Asp
        525

TGGCTGCTTA GAGTCAGCCT GGGTGGCACC AGGCAATGCA GGTGAAGTGG CTGCCTTCAG 1759
```

FIG. 6F

```
GAAATACAAC TAACTAAAAT CAAACACCTA GGTCACGTGC CTCTCAAATA CTGATTTCTG 1819
CCACAGCACC TCTTGAGGCA TCCCTTGGCT ATTCTGTGCA TATTGTTCTT CAGAGACCTC 1879
ACTACCCACA TGCTGATCTA TTGGGGAACA GAGAAGAGAC AGGCCACTAA GGTCAGGCTC 1939
TTTATATTAA GTTCCCCAGA GGAAGAGTAA GTTGAGAAGG TATCAGTTTA ATGTTGAAGA 1999
ATTGACCTCA GGGCTCAGTT TCCATTTCCC TCCCTCAGTA TTCTTCCTGG CAAGATACCC 2059
ATTAAGCATT TCGCCAATCA GAATCTCATT TTATAGTTTT TCCCATTGGT CTTTAACTAA 2119
GACTTTCTTG TAGCAATCTC GTAAGCAGTG AACCCCCTCA GATCAGTAGA ATATAGTATC 2179
TGGGGGAGAA GACTTACTTC CTTCAGGGCA GCAGCCACAG CCAGGCTTCT GTCATACAGG 2239
TAGATCCCGA AGCACAGAGA CATAAAAAAG GTCTCCCAGA AAACTATAGA CCATTCTCCA 2299
AGTGGAATTC CCACTTAGGG CTCTGGTCAC TAGATTGCAA CCTGTGTGTT TGTCATCATC 2359
CTCATCTCAC CATTGTATTG CTATGCCCTC CCATAAAAAC ACATTGATCC CTAGCAAGAT 2419
```

FIG. 6G

```
TATTGCATTC CAGATTTTAC TGCCTTTGCT AGGCTTTTGC TTAGCAAAGG GCTGACTTTC 2479
CATTGTTATC ATGGTGTATA TATTTTTGTC ACCATTCCCA CAAGTATACT TGATGTTGTC 2539
ATAGAACGAA CATCCTACTC TATGATTTAC TAACCAATTA CTTTCCCAGA TCATAGACCT 2599
CTCTGCATAG TAGTCATAGG TCTTGACTTT GGGGAAAGAA AAGGAAGCTG CAGGAATATT 2659
TATCTCCAAA GTCGAATGAG AAAGAACTCC AGCAAATCCA ATGGCTACAA ACTAAAAATC 2719
AGCATTATTT CATATTGCTG TTTCTTAGCT GAATATGGAA TAAAGAACTA TTATTTTATT 2779
TTGAAAAAAA AAAAAAAA                                               2797
```

FIG. 6H

```
GCGCGCGCGT TTTCCTTGTT CCTGGTCAAC AAAGAAATGT GGAGTGTCTT GGCTGAATCC 60

TCATACAGAC AAGATCATTA TGGTGCTGTT AGGTAGGACT TGTATCCAGA TGTAAGGTTG 120

AAAAAGTGAT ATAATAAAGG AACCAAGGAG AAAATTCAGA AGGAAAGAAA AAATTGCCTC 180

TGCAGGTGTG CGAGCAGGAT TGCTTCTGCA ACAAAAGCCT CCACCCAGCC ACATCTTGGG 240

AAAAGA ATG GCC ACT TCT TGG GGC ACA GTC TTT TTC ATG CTG GTG GTA    288
       Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val
        1               5                  10

TCC TGT GTT TGC AGC GCT GTC TCC CAC AGG AAC CAG CAG ACT TGG TTT    336
Ser Cys Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe
 15                  20                  25                  30

GAG GGT ATC TTC CTG TCT TCC ATG TGC CCC ATC AAT GTC AGC GCC AGC    384
Glu Gly Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser
                 35                  40                  45

ACC TTG TAT GGA ATT ATG TTT GAT GCA GGG AGC ACT GGA ACT CGA ATT    432
Thr Leu Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile
             50                  55                 60
```

FIG. 7A

```
CAT GTT TAC ACC TTT GTG CAG AAA ATG CCA GGA CAG CTT CCA ATT CTA   480
His Val Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu
         65                  70                  75

GAA GGG GAA GTT TTT GAT TCT GTG AAG CCA GGA CTT TCT GCT TTT GTA   528
Glu Gly Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val
     80                  85                  90

GAT CAA CCT AAG CAG GGT GCT GAG ACC GTT CAA GGG CTC TTA GAG GTG   576
Asp Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val
 95                 100                 105                 110

GCC AAA GAC TCA ATC CCC CGA AGT CAC TGG AAA AAG ACC CCA GTG GTC   624
Ala Lys Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val
                115                 120                 125

CTA AAG GCA ACA GCA GGA CTA CGC TTA CTG CCA GAA CAC AAA GCC AAG   672
Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys
            130                 135                 140

GCT CTG CTC TTT GAG GTA AAG GAG ATC TTC AGG AAG TCA CCT TTC CTG   720
Ala Leu Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu
        145                 150                 155
```

FIG. 7B

```
GTA CCA AAG GGC AGT GTT AGC ATC ATG GAT GGA TCC GAC GAA GGC ATA    768
Val Pro Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile
    160                 165                 170

TTA GCT TGG GTT ACT GTG AAT TTT CTG ACA GGT CAG CTG CAT GGC CAC    816
Leu Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His
175                     180                 185                 190

AGA CAG GAG ACT GTG GGG ACC TTG GAC CTA GGG GGA GCC TCC ACC CAA    864
Arg Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln
                195                 200                 205

ATC ACG TTC CTG CCC CAG TTT GAG AAA ACT CTG GAA CAA ACT CCT AGG    912
Ile Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg
            210                 215                 220

GGC TAC CTC ACT TCC TTT GAG ATG TTT AAC AGC ACT TAT AAG CTC TAT    960
Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr
        225                 230                 235

ACA CAT AGT TAC TTG GGA TTT GGA TTG AAA GCT GCA AGA CTA GCA ACC   1008
Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr
    240                 245                 250
```

FIG. 7C

```
CTG GGA GCC CTG GAG ACA GAA GGG ACT GAT GGG CAC ACT TTC CGG AGT    1056
Leu Gly Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser
255                 260                 265                 270

GCC TGT TTA CCG AGA TGG TTG GAA GCA GAG TGG ATC TTT GGG GGT GTG    1104
Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val
                275                 280                 285

AAA TAC CAG TAT GGT GGC AAC CAA GAA GGG GAG GTG GGC TTT GAG CCC    1152
Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro
            290                 295                 300

TGC TAT GCC GAA GTG CTG AGG GTG GTA CGA GGA AAA CTT CAC CAG CCA    1200
Cys Tyr Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro
        305                 310                 315

GAG GAG GTC CAG AGA GGT TCC TTC TAT GCT TTC TCT TAC TAT TAT GAC    1248
Glu Glu Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp
    320                 325                 330

CGA GCT GTT GAC ACA GAC ATG ATT GAT TAT GAA AAG GGG GGT ATT TTA    1296
Arg Ala Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu
335                 340                 345                 350
```

FIG. 7D

```
AAA GTT GAA GAT TTT GAA AGA AAA GCC AGG GAA GTG TGT GAT AAC TTG   1344
Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu
                355                 360                 365

GAA AAC TTC ACC TCA GGC AGT CCT TTC CTG TGC ATG GAT CTC AGC TAC   1392
Glu Asn Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr
            370                 375                 380

ATC ACA GCC CTG TTA AAG GAT GGC TTT GGC TTT GCA GAC AGC ACA GTC   1440
Ile Thr Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val
        385                 390                 395

TTA CAG CTC ACA AAG AAA GTG AAC AAC ATA GAG ACG GGC TGG GCC TTG   1488
Leu Gln Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu
    400                 405                 410

GGG GCC ACC TTT CAC CTG TTG CAG TCT CTG GGC ATC TCC CAT           1530
Gly Ala Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His
415                 420                 425

TGAGGCCACG TACTTCCTTG GAGACCTGCA TTTGCCAACA CCTTTTTAAG GGGAGGAGAG 1590
```

FIG. 7E

```
AGCACTTAGT TTCTGAACTA GTCTGGGACA TCCTGGACTT GAGCCTAGAG ATTTAGGTTT 1650
AATTAATTTT ACACATCTAA TGTGAACTGC TGCCTAACCA CTCAAGAGTA CACAGCTGGC 1710
ACCAGAGCAT CACAGAGAGC CCTGTGAGCC AAAAAGTATA GTTTTGGAAC TTAACCTTGG 1770
AGTGAGAGCC CAGGGACAGG TCCCTGGAAA CCAAAGAAAA ATCGCATTTC AACCCTTTGA 1830
GTGCCTCATT CCACTGAATA TTTAAATTTT CCTCTTAAAT GGTAAACTGA CTTATTGCAA 1890
TCCCAAGACC CATCAATATC AGTATTTTTT TCCTCCCTAT ACAGTGCCCT GCCCACCCTT 1950
ATCTGCACCC ACCTCCCCTG AAAAAGAGAG AAAAAAAAAA AAAAAAAA                1998
```

FIG. 7F

```
CD39L2    1  MKKGIRYETSRKTSYIFQQPQHGPWQTRMRKISNHGSLRVAKVAYPLGLCVGVFIYVAYI
CD39L4    1  ------------------------------------------------------MATSWG
CD39L1    1  ------------------------------------------------------------
CD39L3    1  ---------------------------------------------MFTVLTRQPCEQAGL
CD39      1  ------------------------------------------------------MEDTKE

                                                             ACR I
CD39L2   61  KWHRATATQAFFSITRAAPGARWGQQAH-SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQ
CD39L4    7  TVFFMLVVSCVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGTRIHVYT
CD39L1    1  ---MAGKVRSLLPPLLLAAAGLAGLLLLCVPTRDVREP?ALKYGIVLDAGSSHTSMFIYK
CD39L3   16  KALYRTPTIIALVVLLVSIVVLVSITVIQIHKQEVL-PPGLKYGIVLDAGSSRTTVYVYQ
CD39      7  SNVKTFCSKNILAILGFSSIIAVIALLAVGLTQNKALPENVKYGIVLDAGSSHTSLYIYK

                                                                 ACR II
CD39L2  120  FT-RPPRETPTLTHETFKAVK-PGLSAYADDVEKSAQGIRELLDVAKQDIPFDFWKATPL
CD39L4   67  FVQKMPGQLPILEGEVFDSVK-PGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHWKKTPV
CD39L1   58  WPADKENDTGIVGQHSSCDVPGGGISSYADNPSGASQSLVGCLEQALQDVPKERHAGTPL
CD39L3   75  WPAEKENNTGVVSQTFKCSVKGSGISSYGNNPQDVPRAFEECMQKVKGQVPSHLHGSTPI
CD39     67  WPAEKENDTGVVHQVEEC/RVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPV
```

FIG. 8A

ACR II ACR III

```
CD39L2  178  VLKATAGLRLL---PGEKAQKLLQKVKEVFKASPFLVGDDCVSIMNGTDEGVSAWITIN
CD39L4  126  VLKATAGLRLL---PEHKAKALLFEVKEIFRKSPFLVPKGSVSIMDGSDEGILAWVTVNF
CD39L1  118  YLGATAGMRLLNLTNPEASTSVLMAVTHTLTQYPF--DFRGARILSGQEEGVFGWVTANY
CD39L3  135  HLGATAGMRLLRLQNETAANEVLESIQSYFKSQPF--DFRGAQIISGQEEGVYGWITANY
CD39    127  YLGATAGMRLLRMESEELADRVLDVVERSLSNYPF--DFQGARIITGQEEGAYGWITINY
```

ACR IV

```
CD39L2  235  LTGSL------------KTPGGSSVGMLDLGGGSTQIAFLPRVEGTLQASPPGYLTALRM
CD39L4  183  LTGQL------------HGHRQETVGTLDLGGASTQITFLPQFEKTLEQTPRGYLTSFEM
CD39L1  176  LLENFIKYGWVGRWF--RPR-KGTLGAMDLGGASTQITFETTSPAEDRASE---V-QLHL
CD39L3  193  LMGNFLEKNLWHMWV--HPHGVETTGALDLGGASTQISFVAGEKMDLNTSD---IMQVSL
CD39    185  LLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDN---ALQFRL
```

```
CD39L2  283  FNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSPSFKGEWEHAEVTYR
CD39L4  231  FNSTYKLYTHSYLGFGLKAARLATLGALETE-GTDGHTFRSACLPRWLEAEWIFGGVKYQ
CD39L1  229  YGQHYRVYTHSFLCYGRDQVLQRLL-ASALQ-----THGFHPCWPRGFSTQVLLGDVYQS
CD39L3  248  YGYVYTLYTHSFQCYGRNEAEKKFL-AMLLQNSPTKNHLTNPCYPRDYSISFTMGHVFDS
CD39    242  YGKDYNVYTHSFLCYGKDQALWQKL-AKDIQVASNEI-LRDPCFHPGYKKVVNVSDLYKT
```

FIG. 8B

```
CD39L2   343   VSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDLAAGVGLIDAEKGGS
CD39L4   290   YGGNQEGEVGFEPCYAEVLRVVRGKLHQPEEVQRGSFYAFSYYYDRAVDTDMIDYEKGGI
CD39L1   283   PCTMAQRPQNFNSSARVSLSGSSDPHLCRDLVSGLFSFSSC-PFSRCSFNGVFQPPVAGN
CD39L3   307   LCTVDQRPESYNPNDVITFEGTGDPSLCKEKVASIFDFKACHDQETCSFDGVYQPKIKGP
CD39     300   PCT--KRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYC-PYSQCAFNGIFLPPLQGD

CD39L2   403   LVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPRSKVLKLTRKIDNVE
CD39L4   350   LKVEDFERKAREVCDNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQLTKKVNNIE
CD39L1   342   FV------AFSAFFYTVDFLRTSMGLPVATLQQLEAAAVNVCNQTWAQ------------
CD39L3   367   FV------AFAGFYYTASALNLSGSF---SLDTFNSSTWNFCSQNWSQLPLLLPKFDEVY
CD39     357   FG------AFSAFYFVMKFLNLTS--EKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKY

CD39L2   462   TSWALGAIFHYIDSLNRQKSPAS*
CD39L4   410   TGWALGATFHLLQSLGISH
CD39L1   384   ------------QLLSRGYGFDERAFGGVIFQKKAADTAVGWALGYMLNLTNLIPADPPG
CD39L3   418   ARSYCFSANYIYHLFVNGYKFTEETWPQIHFEKEVGNSSIAWSLGYMLSLTNQIPAESPL
CD39     409   LSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQP-
```

FIG. 8C

CD39L2	485	
CD39L4	429	
CD39L1	432	L R K G T D F S S W V V L L L L F A S A L L A A L V L L L R Q V H S A K L P S T I *
CD39L3	478	I R L P I E P P V F V G T L A F F T V A A L L C L A F L A Y L C S A T R R K R H S E H A F D H A V D S D *
CD39	468	L S T P L S H S T Y V F L M V L F S L V L F T V A I I G L L I F H K P S Y F W K D M V *

FIG. 8D

```
peaGDP     1   ----------------------------------------------------------M
potapyrase 1   ------------------------------------------------------MLNQN
CD39L2     1   MKKGIRYETSRKTSYIFQQPQHGPWQTRMRKISNHGSLRVAKVAYPLGLCVGVFIYVAYI
CD39L4     1   ------------------------------------------------------MATSWG
dNTPase    1   ------------------------MKYEYKLLATDEKPPRRKSSGSPNASSGGNRGPSGL
yGDPase    1   --------------------------------------------------------KTPE

                                                               ACR I
peaGDP     2   ELLIKLITFLLFSMPAITSSQYLGNNL-LTSRKIFLKQEEISSYAVVFDAGSTGSRIHVY
potapyrase 6   SHFIFIILAIFLVLPLSLLSKNVNAQI-PLRRHLLSHESE--HYAVIFDAGSTGSRVHVF
CD39L2     61  KWHRATATQAFFSITRAAPGARWGQQA-H-SPLGTAADGHEVFYGIMFDAGSTGTRVHVF
CD39L4     7   TVFFMLVVSCVCSAVSHRNQQTWFEGI-FLSSMCPINVSASTLYGIMFDAGSTGTRIHVY
dNTPase    37  KISFLCLIISVILLLFVFGFVSENASP-YLARLASKFGYSKVQYAAIIDAGSTGSRVLAY
yGDPase    5   DISILPVNDEPGYLQDSKTEQNYPELADAVKSQTSQTCSEEHKYVIMIDAGSTGSRVHIY
```

FIG. 9A

ACR II

```
peaGDP      61   HFNQNLDLLHIGKGVEYYNKITPGLSSYANNPEQAAKSLIPLLEQAEDVVPDDLQPKTPV
potapyrase  63   RFDEKLGLLPIGNNIEYFMATEPGLSSYAEDPKAAANSLEPLLDGAEGVVPQELQSETPL
CD39L2      119  QFT-RPPRETPTLTHETFKAVKPGLSAYADDVEKSAQGIRELLDVAKQDIPFDFWKATPL
CD39L4      66   TFVQKMPGQLPILEGEVFDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHWKKTPV
dNTPase     96   KFNRSFIDNKLVLYEELFKERKPGLSSFADNPAEGAHSIKLLLDEARAFIPKEHWSSTPL
yGDPas      65   KFD--VCTSPPTLLDEKFDMLEPGLSSFDTDSVGAANSLDPLLKVAMNYVPIKARSCTPV
```

ACR II ACR III

```
peaGDP      121  RLGATAGLRLLNGDASEKILQSVRDMLSNRSTF-NVQPDAVSIIDGTQEGSYLWVTVNYA
potapyrase  123  ELGATAGLRMLKGDAAEKILQAVRNLVKNQSTF-HSKDQWVTILDGTQEGSYMWAAINYL
CD39L2      178  VLKATAGLRLLPGEKAQKLLQKVKEVFK-ASPF-LVGDDCVSIMNGTDEGVSAWITINFL
CD39L4      126  VLKATAGLRLLPEHKAKALLFEVKEIFR-KSPF-LVPKGSVSIMDGSDEGILAWVTVNFL
dNTPase     156  VLKATAGLRLLPASKAENILNAVRDLFA-KSEF-SVDMDAVEIMDGTDEGIFSWFTVNFL
yGDPase     123  AVKATAGLRLLGDAKSSKILSAVRDHLEKDYPFPVVEGDGVSIMGGDEEGVFAWITTNYL
```

FIG. 9B

ACR IV

```
peaGDP     180 LGNLGKKYTK--TVGVIDLGGGSVQMAYAVSKKTAKNAPKVADGDDPYIKKVVLKGIPYD
potapyrase 182 LGNLGKDYKS--TTATIDLGGGSVQMAYAISNEQFAKAPQNEDG-EPYVQQKHLMSKDYN
CD39L2     236 TGSLKTPGGS--SVGMLDLGGGSTQIAFLPRVEG-----TLQASPPGYLTALRMFNRTYK
CD39L4     184 TGQLHGHRQE--TVGTLDLGGASTQITFLPQFEK-----TLEQTPRGYLTSFEMFNSTYK
dNTPase    214 LGRLSKTNQA--AA--LDLGGGSTQVTFSPTDPD-----QVPVYDK-YMHEVVTSSKKIN
yGDPase    183 LGNIGANGPKLPTAAVFDLGGGSTQIVFEPTFPINEKMV-----DGEHKFDLKFGDENYT

peaGDP     238 LYVHSYLHFGREASRAEILKLTPRSP------------------NPCLLAGFNG----IY
potapyrase 239 LYVHSYLNYGQLAGRAEIFKASRNES------------------NPCALEGCDG----YY
CD39L2     289 LYSYSYLGLGLMSARLAILGGVEGQPAKDGKELV----------SPCLSPSFKG---E-W
CD39L4     237 LYTHSYLGFGLKAARLATLGALETE-GTDGHTFR----------SACLPRWLEA---E-W
dNTPase    264 VFTHSYLGLGLMAARHAVF---THGYKKEDTVLE----------SVCVNPIIAN---RTW
yGDPase    238 LYQFSHLGYGLKEGRNKVNSVLVENALKDGKILKGDNTKTHQLSSPCLPPKVNATNEKVT
```

FIG. 9C

```
peaGDP      276  TYSGEEFKATAYTSG-ANFNKCKNTIRKALKLNYPCPYQNCTFGGIWNGG---GGNGQKN
potapyrase  277  SYGGVDYKVKAPKKG-SSWKRCRRLTRHALKINAKCNIEECTFNGVWNGG---GGDGQKN
CD39L2      335  EHAEVTYRVSGQKAAASLHELCAAR---VSEV-----LQNRV-----HRT---EEVKHVD
CD39L4      282  IFGGVKYQYGGNQEGEVGFEPCYAE---VLRV-----VRGKL-----HQP---EEVQRGS
dNTPase     308  TYGNVQYKVSGKENGKSSAEQPIVDFDACLEL-----VKSKVMPLVKPKP---FTLKQHA
yGDPase     298  LESKETYTIDFIGPDEPSGAQCRFLTDEILNKDAQCQSPPCSFNGVHQPSLVRTFKESND

peaGDP      332  LFASSSFFYLPEDTGMVDASTPNFILRPVDIETKAKEACALNFEDAKSTYPFLDKKNVAS
potapyrase  333  IHASSFFYDIGAQVGIVDTKFPSALAKPIQYLNAAKVACQTNVADIKSIFPKTQDRNI-P
CD39L2      379  FYAFSYYYDLAAGVGLIDAE-KGGSLVVGDFEIAAKYVCRT----------LETQPQSSP
CD39L4      326  FYAFSYYYDRAVDTDMIDYE-KGGILKVEDFERKAREVCDN----------LENFTSGSP
dNTPase     360  VAAFSYYFERAIESGLVDPL-AGGETTVEAYRKKAQEICAI----------PNDE---QP
yGDPase     358  IYIFSYFYDRTRPLGMPLSFTLNELNDLARIVCKGEETWNSVFSGIAGSL---DELESDS
```

FIG. 9D

```
peaGDP      392  YVCMDLIYQYVLLVDGFGLDPLQKITSGKEIEYQDAIVEAAWPLGNAVEAISALPKFERL
potapyrase  392  YLCMDLIYEYTLLVDGFGLNPHKEITVIHDVQYKNYLVGAAWPLGCAIDLVSSTTNKIRV
CD39L2      428  FSCMDLTYVSLLLQE-FGFPRSKVLKLTRKIDN----VETSWALGAIFHYIDSLNRQKSP
CD39L4      375  FLCMDLSYITALLKDGFGFADSTVLQLTKKVNN----IETGWALGATFHLLQSLGISH
dNTPase     406  FMCFDLTFISTLLREGFGLNDGKKIKLYKKIDG----HEISWALGCAYNVLTSDEKFSNS
yGDPase     415  HFCLDLSFQVSLLHTGYDIPLQRELRTGKKIANK----EIGWCLGASLPLLKADNWKCKI

peaGDP      452  MYFV
potapyrase  452  ASS*
CD39L2      483  AS*
CD39L4      429
dNTPase     462
yGDPase     471  QSA
```

FIG. 9E